

The predicted protein sequences of Cssl (A), Hydrophobin (B), GAPDH-B (C), enolase (D), catalase B (E), catalase A (F), and isopropylmalate dehydrogenase B (G). X₁ is S or A and X₂ is L or I.

A
MLASFQFCILPRTYRTLLCSAGAGPLLIQFVTVASALALAPTAVVARQGAAAFVTVNSIDVCPKKVAQEIIINPGPKVVTTP
YTCDQVKLGHGLDVSYYNFDIEPLTKDTFPYCKALKVFDNEGCLGFPPLTWI PLESPLDKCIPEHYFSDEVKSI SFQLDCRE
DAPVKKPEPYGPKGAEQSAQAHEHSTKQDAQQGS HQGQEVQNSPKQEARQGS RPAEAPKQEQAQAEQAASEAPEKKASNPAD
SLGLGELTKVLGFR

B
VRFVPDDITVKQATEKCGDQAQLSCCNKATYAGDVTIDIDEGILAGTLKNLIGGGSGTEGLGLFNQCSKLDLQSPIIGIPIQ
DLVNQCKQNIACCQNSPSDAVRFP

C
MATPKVGINGFGRIGRIVGLNSLSHGVDVAVNDPPIEVHYAAYMLKYDTTHGQFKGTIETYDQGLIVNGKKIRFYAEKD
PSQIPWSETGAAYIVESTGVFTTKEKASAHKGGAKKVIISAPSADAPMFVMGVNNTTYTSDIQVLSNASCCTTNCLAPLA
KVINDKFGIVEGLMTTVHSYTATQKVVDAPSNDWRGGRATAQNIIPSSGTAAKAVGKVI PSLNGKLTGMAMRVPTSNVS
VVDLTCRLEKGASYDEIKQAIKAASEEGELKNILGYTEDDVSSDLNGDERS SIFDAKAGISLNPNFVKLVAWYDNEW

D
MPISKIHARSVYDSRGNPTVEVDVATETGLHRAIVPSGASTGQHEAHEL RDGDKTQWGGKGVLKAVKNVNETIGPALIKENI
DVKDQSKVDEFLNKLDGTANKSNLGANAILGVSLAVAKAGAAEKGVPLYAHISDLAGTKKPYVLPVPFQNVNLNGGSHAGGRL
AFQEFMIVPDSAPSFSEALRQGADEVYQKLKALAKKKYQGSAGNVGDEGGVADPIQTAEALDLITEAIEQAGYTGK
IKIAMDVASSEFYKADVKKYDLDFKNPESDPSKWLTYEQLADLYKSLAAKYPIVSIEDPFAEDDWEAWSFYKTSDFQIVGD
DLTVTNPGRIKKAIELKSCNALLKVNQIGTLTESIQAAKDSYADNWGMVMSHRSGETEDVTIADIAGLRSQG IKTGAPCR
SERLAKLNQILRIEELGENTVYAGSKFR TAVNL

E
MRLTFIPSLIGVANAVCPYMTGELNRRDEISDGAATAEFLSQYYLNDNDAFMTSDVGGPIEDQNSLSAGERGPTLLED F
IFRQKIQRFDHERVPERAVHARGAGAHGVFTSYGDFS NITAASFLAKEGKQTPVVFVRFSTVAGSRGSSDLARDVHGFA TRFY
TDEGNFDIVGNNIPVFFIQDAILF PDLIHAVKPRGDNEIPQAATAHDSAWDFFSQQPSTMTLLWAMSGHGI PRSF
RHVDGFGVHTFRFVTDGASKLVKFHWKSLQKASMWEEAQTSKGNPDFMRQDLHDAIEAGRYPEWELGVQIMDEEDQLR
FGFDLLDPTKIVPEEFVPIITLKGKMLNRNPRNYFAETE QVMFQPGHIVRGVDFTEDP LLQGR LFSYLD TQLNRHGGENFEQ
LPINQPRVPVHNNNRD GAGQMF IPLNPHAYS PKTSVNGSPKQANQTVGDGFF TAPGR TSGKLVRVAVSSSFEDVWS
QPRLFYNSLVPAEKQFVIDAIRFENANVKS P VVKNVVIQLNRIDNDLARRVARAIGVAEPEPDPTFFYHNKNTADVGTFG TK
LKKLDGLKVGVLGVSQHPGSGVEGASTLRDRLKDDGVDVVLVAERLADGVDQTYSTSDAIQF DAVVVAAGAESLFAASSFTG G
SANSASGASSLYPTGRPLQILIDGFRFGKTVGALGSGTAALRNAGIATSRDGVYVAQSVTDDFANDLKEGLRTFKF
LDRFPVDH

F
MATKIAGGLHRAQEV LQNTSSKSKKLVDLERDTADAHTQQLTTDHGVRVSN TDQWLRVTNDRRTGPSLLEDQIAREKIH RF
DHERIPERVVHARGTGAFGNFKLKESIEDLTYAGVLTDTSRNTFV FVRFSTVQSGSRGSADTVRDVRGFAVKFYTDEGNWDIV
GNNIPVFFIQDAVKFPDFVHAVKPEPHNEVPQAQTAHN NFWD FVYLHPEATHMFMWAMSDRAIPRSYRMMQGFVGN
TFALVNKEGKRHFVKFHWI PHLGVHSLVWDEALKLGGQDPDFHRKDLMEAI DNKAYPKWDFAIQV IPEEKQDDFEFDILDAT
KIWPENLVPLRVIGELELNRRNVDEFFPQTEQVAFCTSHIVPGIDFTDDP LLQGRNFSYFDTQISRLGINWEELPINRPVCPV
LNHNRDGQMRHRTQGT VNYWPNRFEAVPPTGTKSGVG GGF TYPQRVEGIKNRALNDKFRHHNQALFYNSMS
EHEKLMHKAFS FELDHCDPTVYERLAGHRLAEIDLELAQKVAEMVGAPIPAKALKQNHGRRAPHL SQTEFIPKNPTIASR
RIAIIGDGYDPVASTGLKTAIKAASALPFIIGTKRS AIYATEDKTSKGIIPDHHDYDQQRSTMF DATFIPGGPHVATLRQN
GQIKYWISETFGHLKALGATGEAVDLVKETLSGTLHVQVASSQSPEPVEWYG VVTAGGKQKPESFKESVQLKGAT
DFVGKFFYQISQHRNYQRELDGLASTIAF

G
MVTYINILVLPDGDGIGPEVMT EAVKVLKVFENEHRKFNLRQELIGGCSIDAHGKS VTEEVKKAAL ESDAVLFAAVGGPKW
DHIRRLDGP EGGLQLRKAMDIYANLRPCSASSPSASIAKEFS PFQREVIEGVDFVVRENC GGAYFGKKIEEEDYAMD
EWGYSEREIQRITRLX₁ AEX₂ ALRHNPPW PVI SLDKANVLASSRLWRRVVEKTM TTEYPQVKLVHQ LADSASLILATNPALN
GVILADNTFGDMISDQAGSIVGTLGLVLP SASLDGLPSETRKRTNGLYEP THGSAPT IAGQNIANP VAMILCVALMFRYSLDM
ETEQRIEKAVQGVLDAGIRTPDLGGKSGTNEVGDAI VAAALQGSS

FIGURE 1

BEST AVAILABLE COPY

The predicted antigenicity indices of CslI (A) and hydrophobin (B) reisdues.

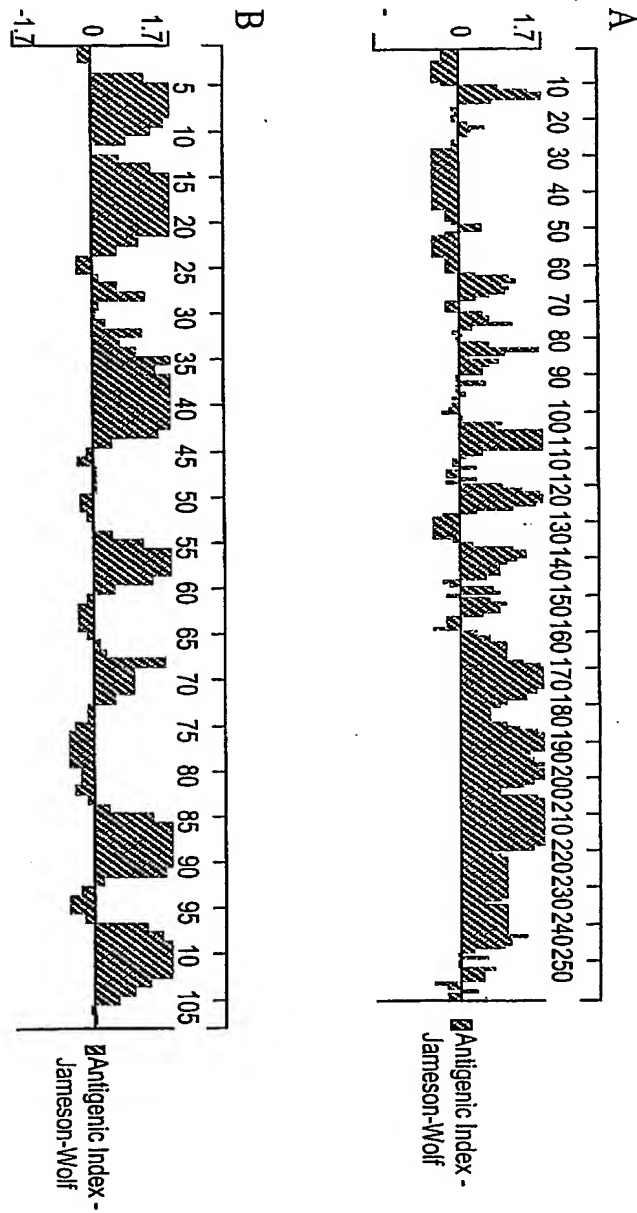


FIGURE 2

Alignment of the predicted protein sequences for GAPDH-A (Afa), GAPDH-B (Afb) and GAPDH-C (Afc).

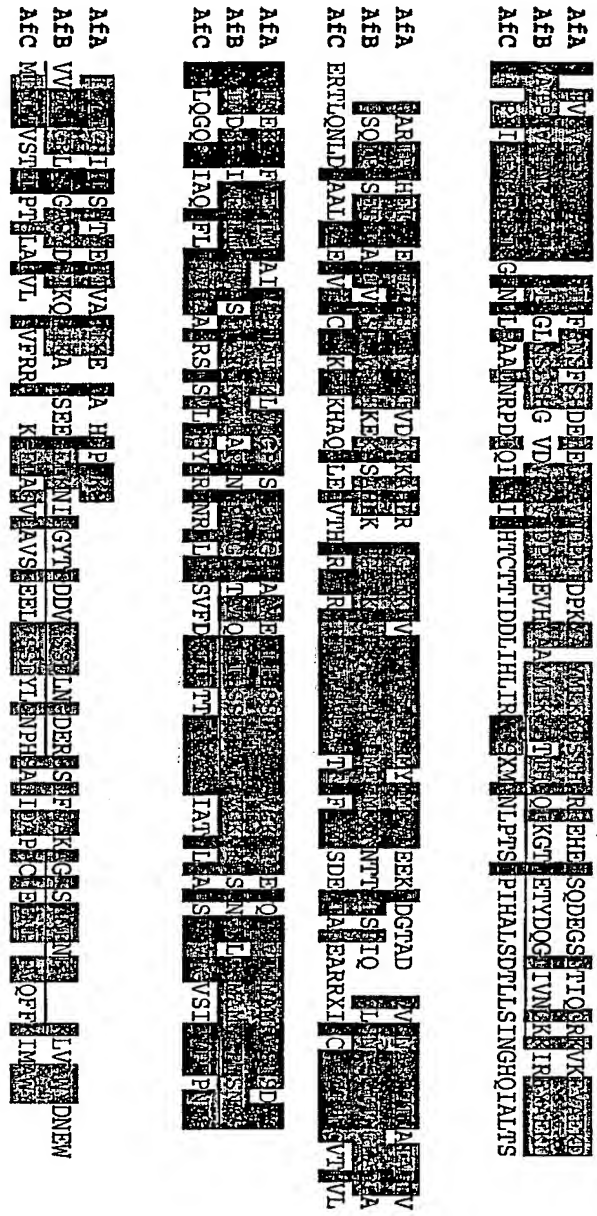


FIGURE 3

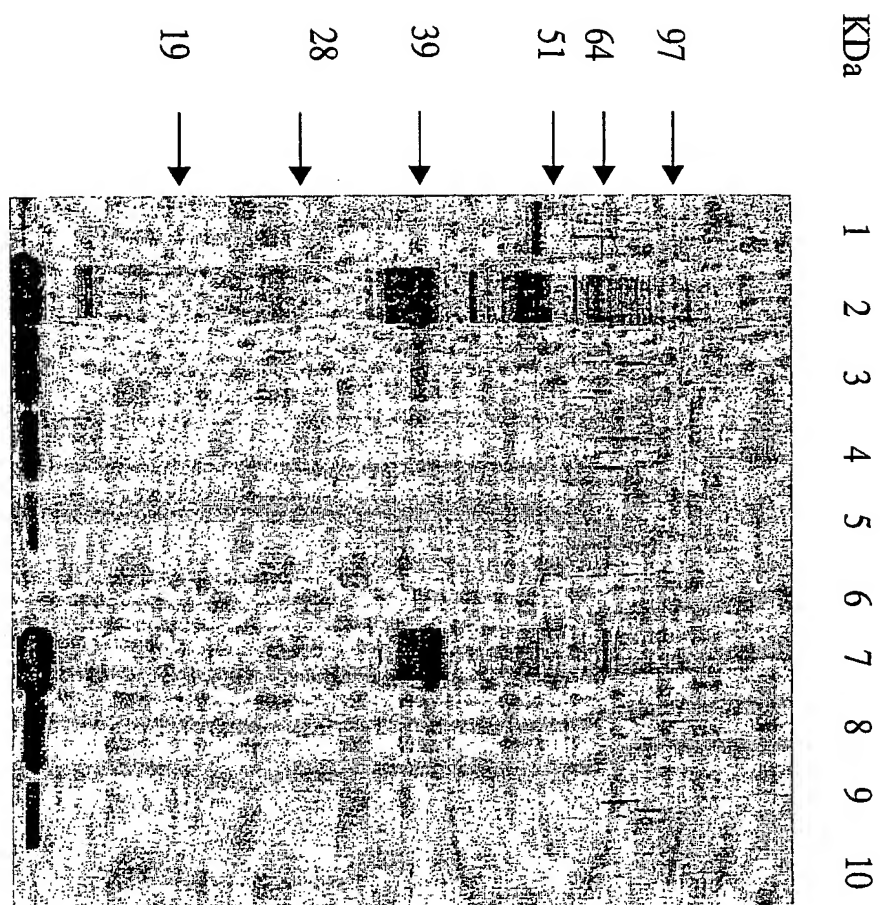


FIGURE 4

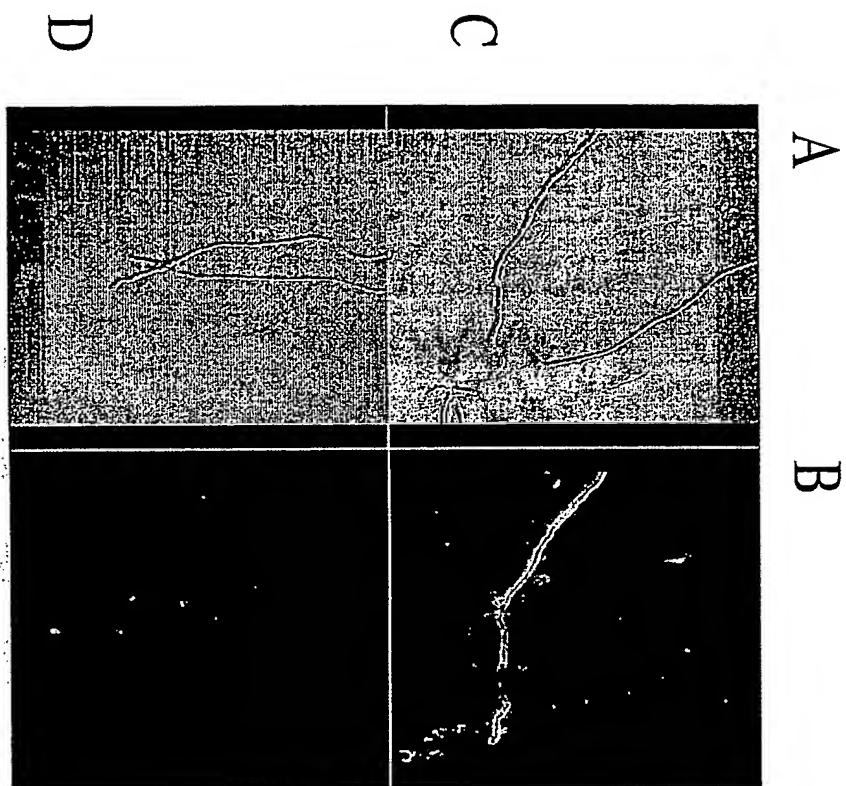


FIGURE 5

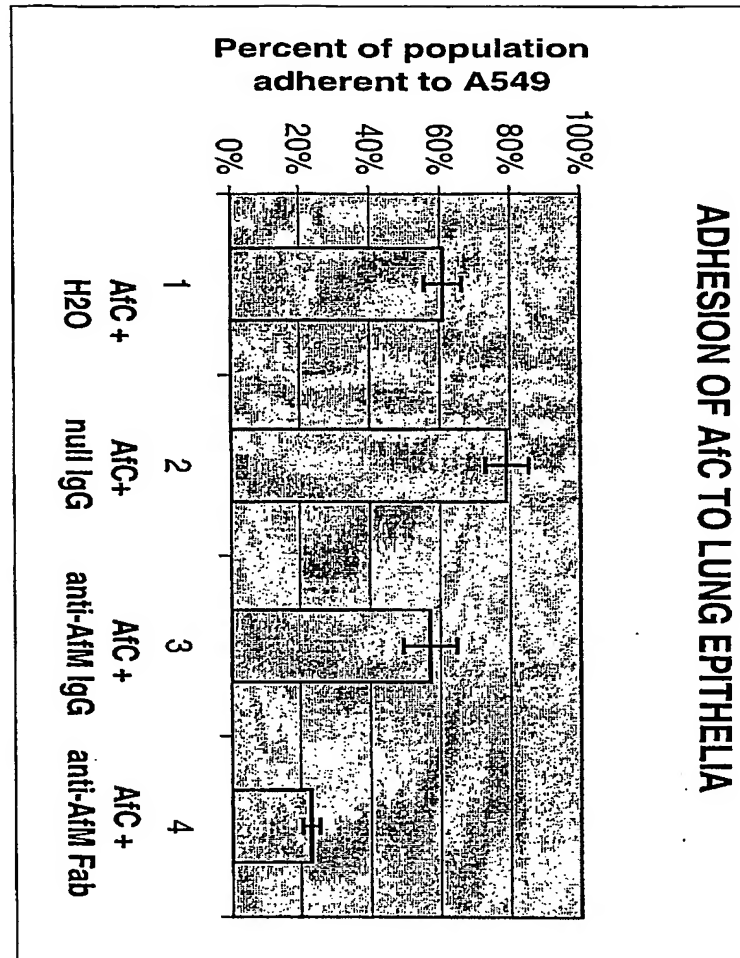


FIGURE 6

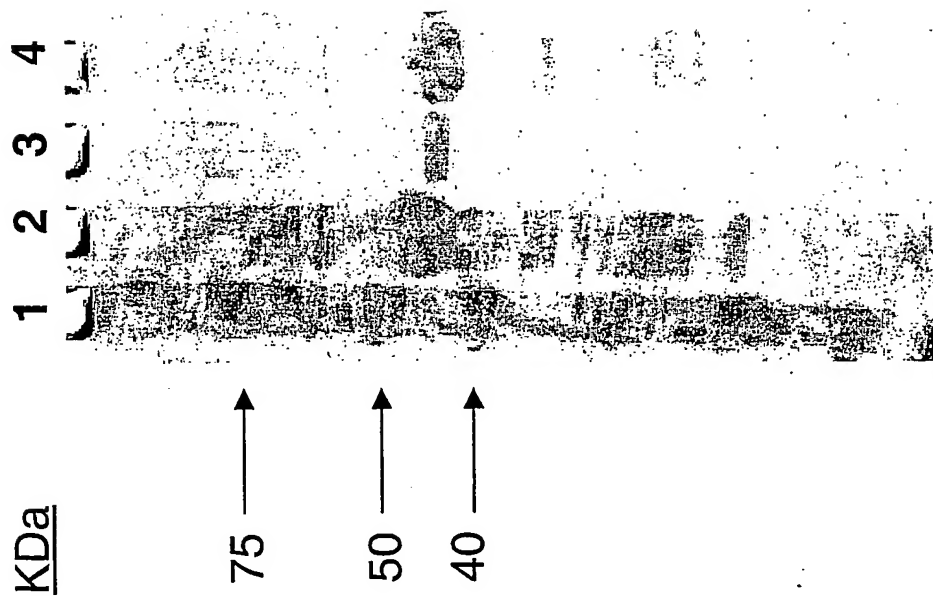


FIGURE 7

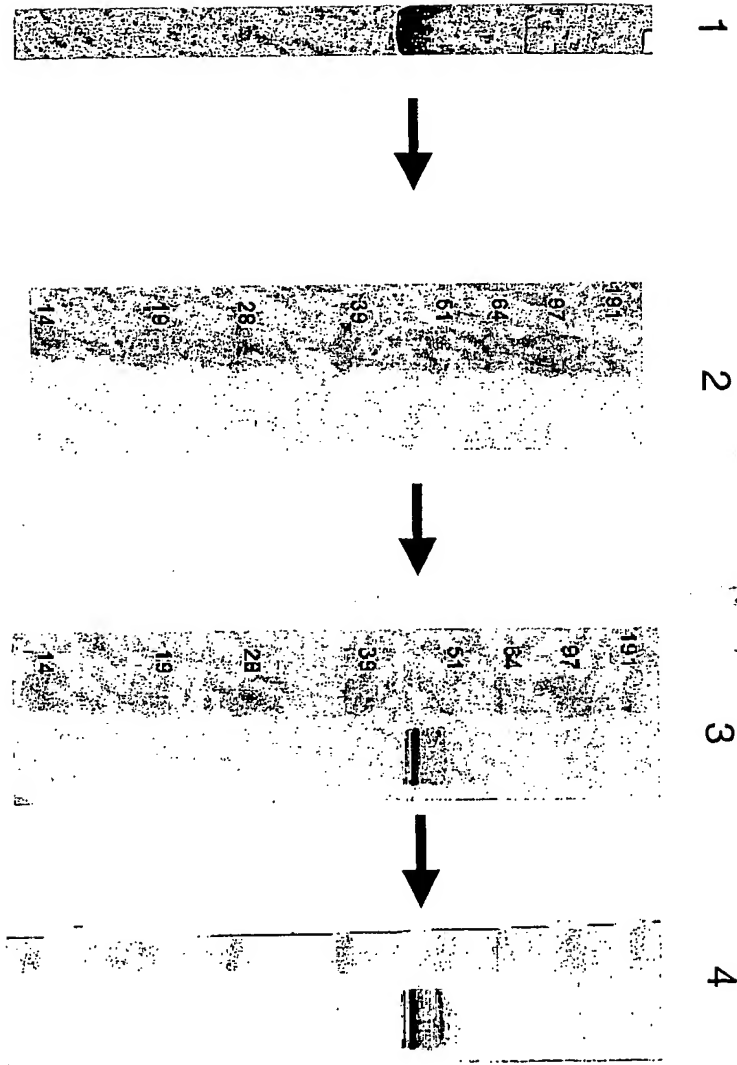


FIGURE 8

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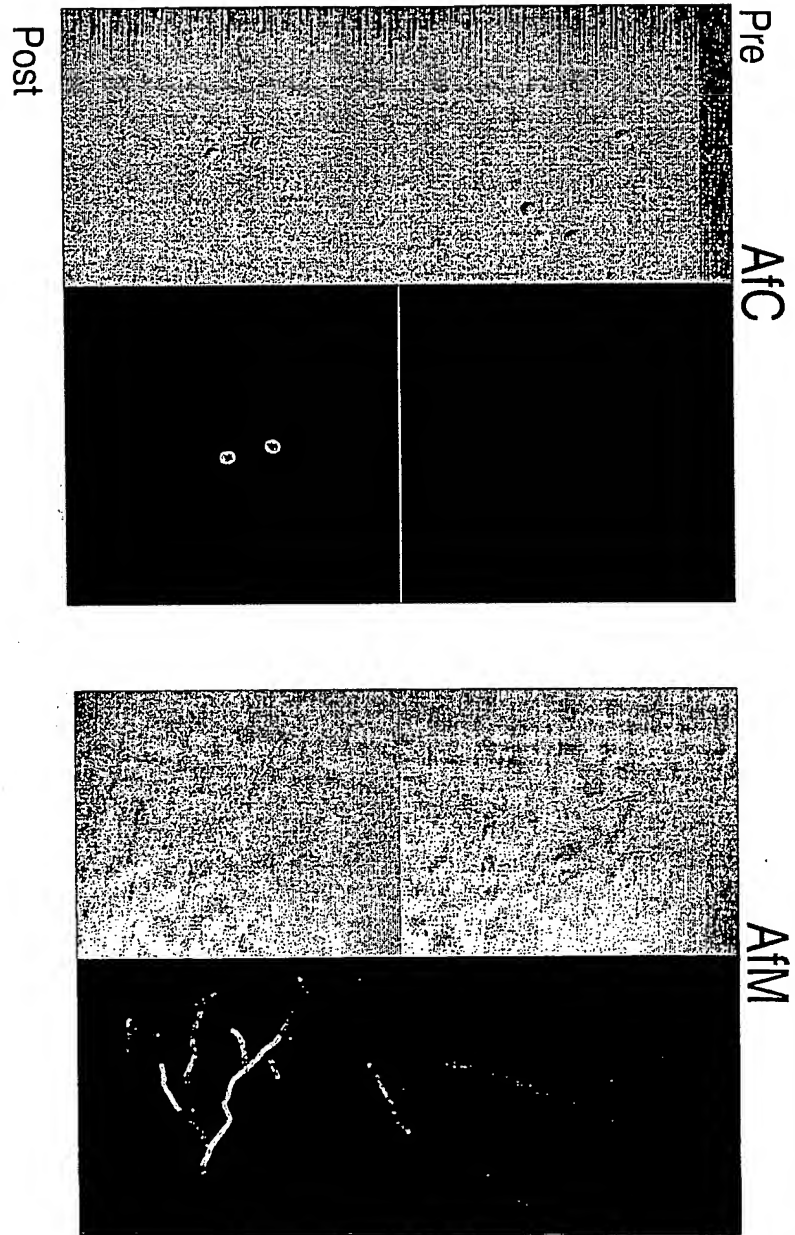


FIGURE 9

10/29

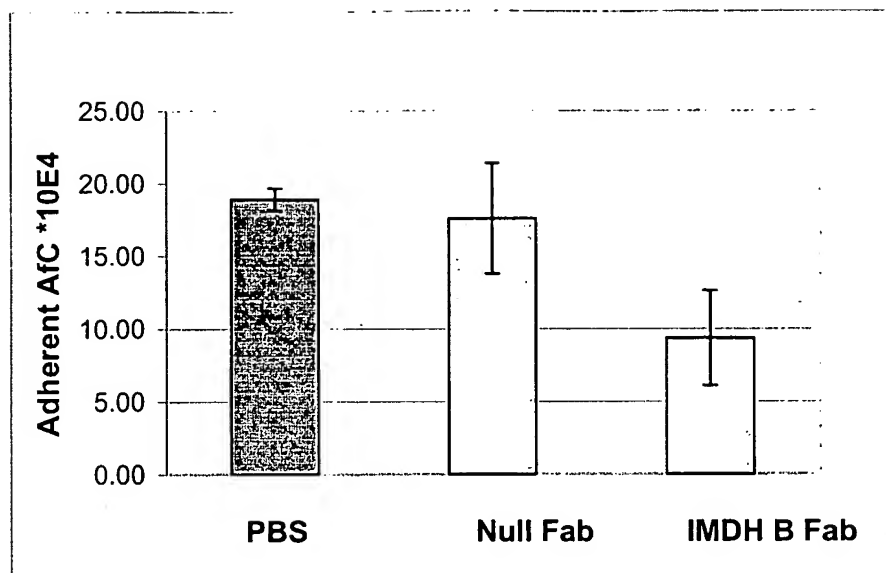


FIGURE 10

11/29

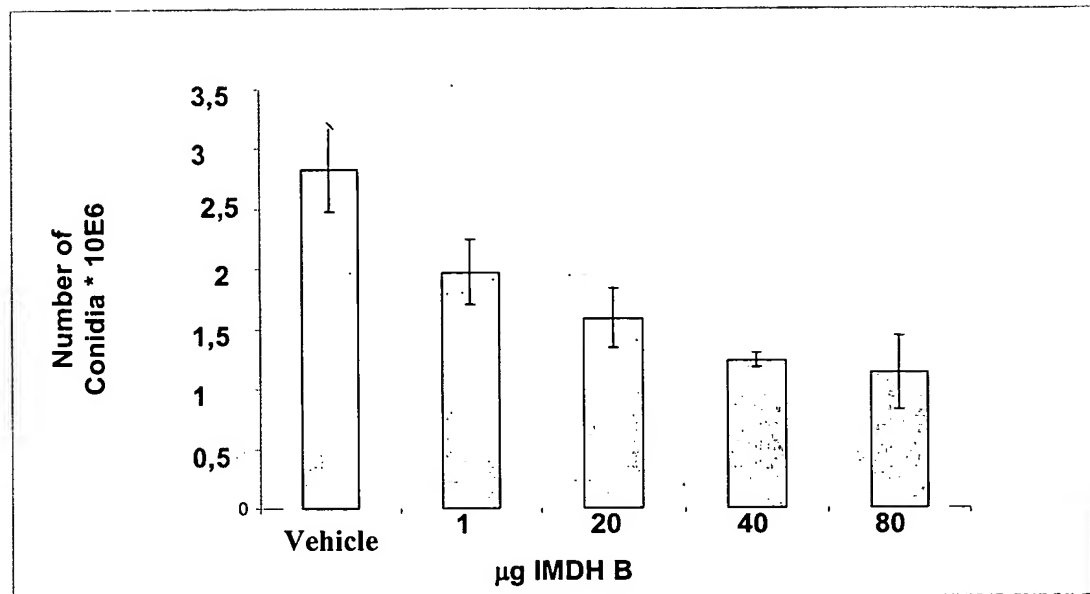


FIGURE 11

12/29

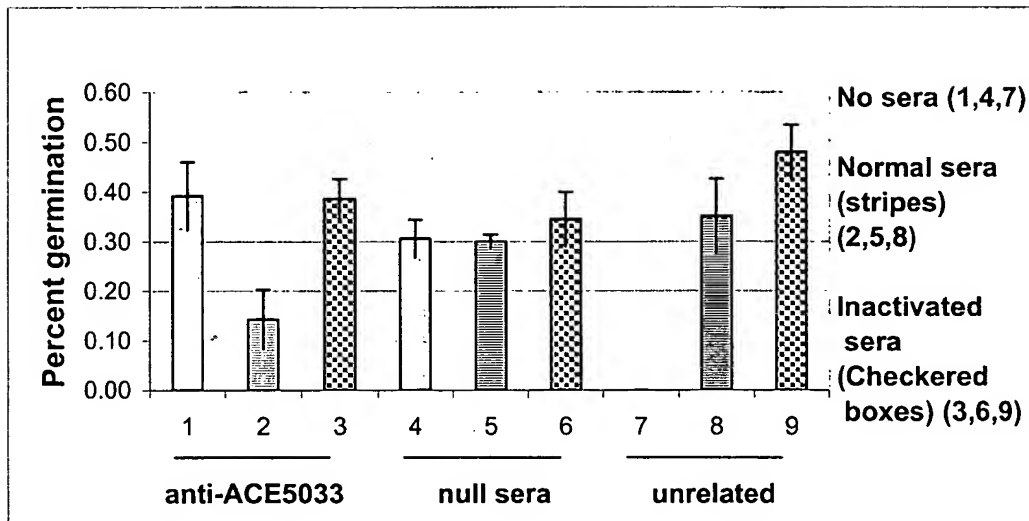
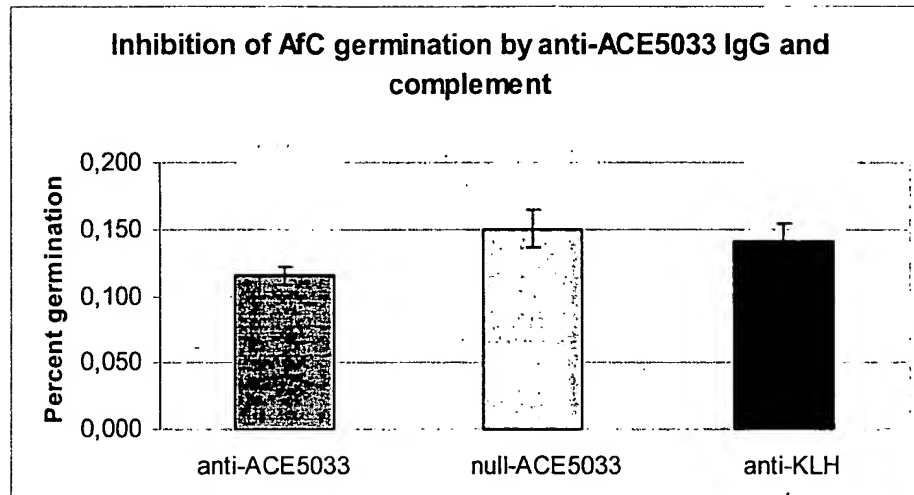


FIGURE 12

**FIGURE 13**

IMDHB1: 3 SYNIVVFAGDHCGPEVSS-----VLRVIEKCRDDATFNLQDQLLGGVSSIDATGSPLTDEA 58
 +YNI+V GD GPEV + VL+V E + FNL+ +L+GG S IDA G +T+E
 IMDHB2: 4 TYNILVLPDGGIGPEVMTEAVKVLKFEN--EHRKFNLRQELIGGCS-IDAHGKSVTEEV 60

 IMDHB1: 59 LNAAKNADAVLLGAIGGPKWG---TGAVRPEQGLLRRLRKEMGTFGNLRPCNFAAPSLV-- 113
 AA +DAVL A+GGPKW G PE GLL+LRK M + NLRPC+ ++PS
 IMDHB2: 61 KKAALSDAVLFAAVGGPKWDHIRRGLDGPPEGGLQLRKAMDIYANLRPCSASSPSASIA 120

 IMDHB1: 114 -DGSPLRPEVCRGVDFNIIRELTGGIYFGDRKEDDGSGFAMDTPEYSRAEIERITRLAAH 172
 + SP R EV GVDF ++RE GG YFG + E++ +AMD YS EI+RITRL+A
 IMDHB2: 121 KEFSPFRQEVIEGVDFVVRNCGGAYFGKKIEED--YAMDEWGYSEREIQRITRLSAE 178

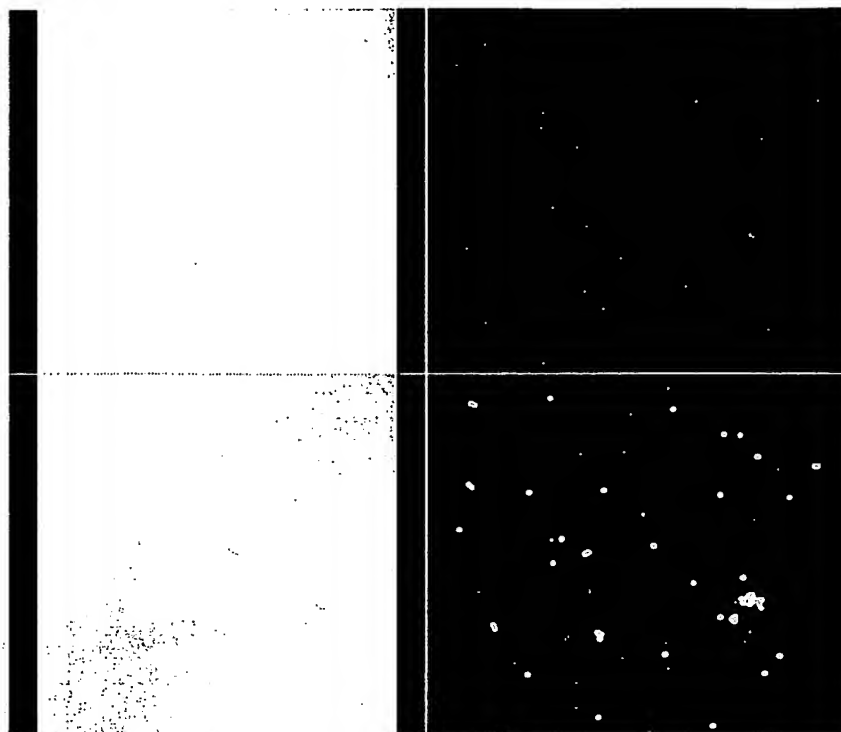
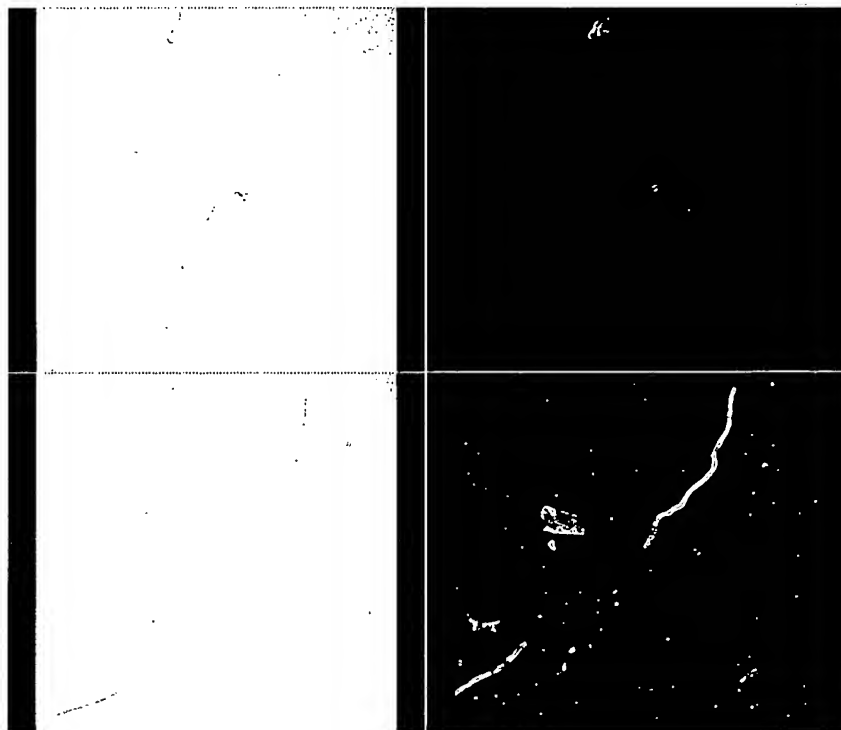
 IMDHB1: 173 LALQHNPPPLPVWSLDKANVLATSRLWRKTVTEVMAKEFPQLKVEHQLIDSAAMIMVKEPR 232
 +AL+HNPP PV SLDKANVLA+SRLWR+ V + M E+PQ+K+ HQL DSA++I+ PR
 IMDHB2: 179 IALRHNPPWPVVISLDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLILATNPR 238

 IMDHB1: 233 KLNGIVVTSNLFGDIISDEASVIPGSLGLLPSASLSGIP-DGKTKVNGIYEPHGSAPDI 291
 LNG+++ N FGD+ISD+A I G+LG+LPSASL G+P + + + NG+YEP HGSAP I
 IMDHB2: 239 ALNGVILADNTFGDMISDQAGSIVGTLGVLPSASLDGLPSETRKRTNGLYEPHGSAPTI 298

 IMDHB1: 292 AGKGIVNPVAAILSVAMMMQYSLNRMDDARAIAETAVRNVIEAGIRTADIGGKSTTSEVGD 351
 AG+ I NPVA IL VA+M +YSL+ +A+ IE AV+ V++AGIRT D+GGKS T+EVGD
 IMDHB2: 299 AGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSGTNEVGD 358

 IMDHB1: 352 AVAAELE 358
 A+ A L+
 IMDHB2: 359 AIVAALQ 365

FIGURE 14

AfC**AfM****FIGURE 15**

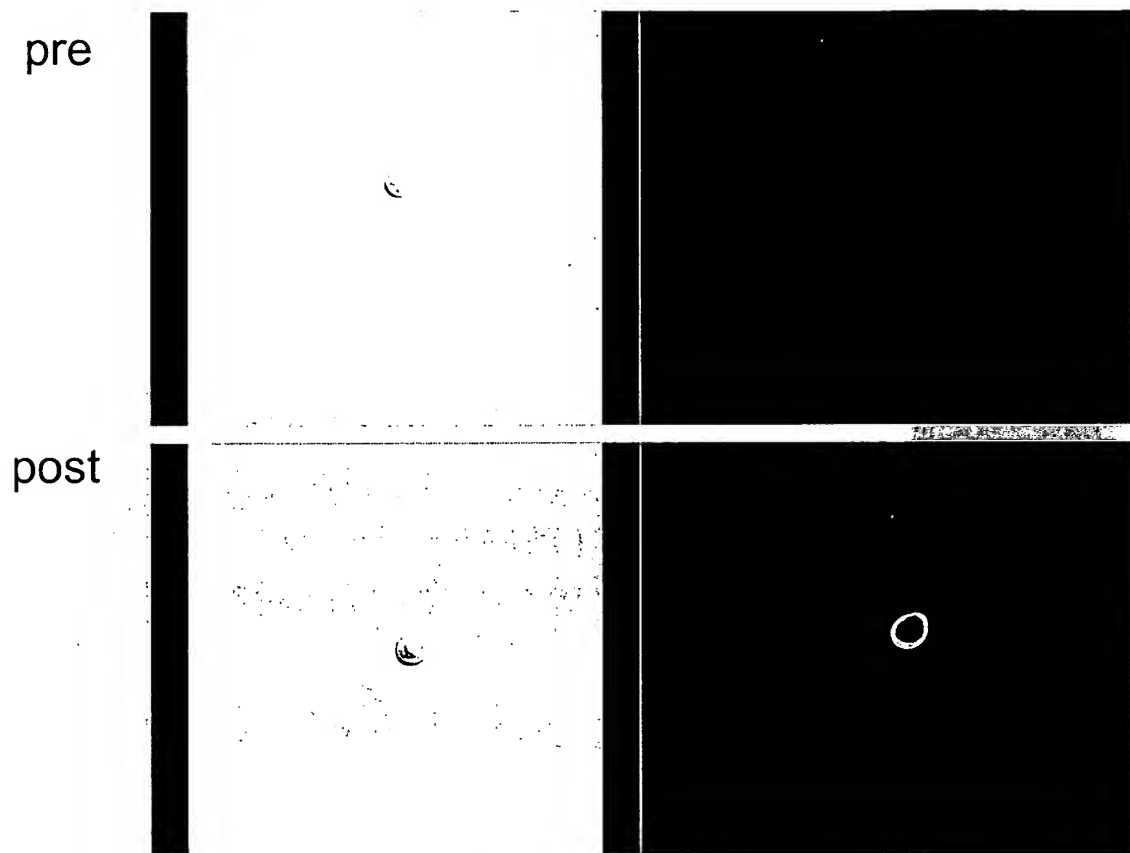


FIGURE 16

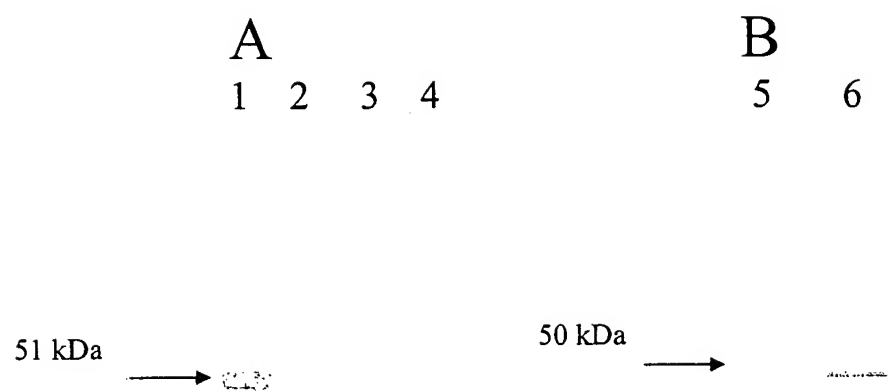


FIGURE 17

BLAST OF SEQ ID NO:36 AGAINST:

Candida orf:

>orf19.7080 orf10262:179916-178795:e 1122 bp, 373 aa, contig 244073 bp
 Length = 1122

Score = 335 bits (860), Expect = 1e-92
 Identities = 185/368 (50%), Positives = 246/368 (66%), Gaps = 9/368 (2%)
 Frame = +1

Query: 2 VTTYNILVLPDGGIGPEVMTEAVKVLKFEN----EHRKFNLRQELIGGCSIDAHGKSVT 57
 V T I VLPD +G E++ EA+KVLK E + +F+ + LIGG +IDA G +
 Sbjct: 7 VKTKTITVLPGDHVGTEIVNEAIKVLKAIEAATPYQKIQFDFKHHLIGGAIDATGVPLP 186

Query: 58 EEVKKAALESDAVLFAAVGGPKWDHIRRGLDGPEGLLQLRKAMDIYANLRPCSASSPSA 117
 ++ ++A SDAVL AVGGPKW G PE GLL++RK +++YAN+RPC+ +S S
 Sbjct: 187 DDALESAKSSDAVLLGAVGGPKWG---TGTVRPEQGLLKIRKELNLYANIRPCNFASDSL 357

Query: 118 SIAKEFSPFRQEVIEGVDFVVRVRENCGGAYFGKKIEEDY-----AMDEWGYSEREIQRI 172
 E SP + EV++G + ++VRE GG YFG++ E+E+ A D Y+ E+ RI
 Sbjct: 358 L---ELSPLKAEVVKGTNLIIVRELVGGIYFGERQEQESEDKKTAWDTEKYTVDEVTRI 528

Query: 173 TRLSAEIALRHNPWPVISLDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLI 232
 TR++A +AL+HNPP P+ SLDKANVLASSRLWR+ V+K ++ E+P + + HQL DSA++I
 Sbjct: 529 TRMAAFMALQHNPPPLPIWSLDKANVLASSRLWRKTVDKVISEEFPAHSVQHQLIDSAAMI 708

Query: 233 LATNPRALNGVILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYEPH 292
 L NP LNG+I+ N FGD+ISD+A I G+LG+LPSASL LP GLYEP H
 Sbjct: 709 LIQNPTKLNGLIITSNMFGDIISDEASVIPGSLGLLPSASLASLPD--TNTAFGLYEPCH 882

Query: 293 GSAPTIAGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSG 352
 GSAP + N NP+A IL A M R SLD EA+ +E+AV+ VLD+GIRT DL G S
 Sbjct: 883 GSAPDLPA-NKVNPIATILSAASMLRLSLDCVKEAEAEAEAVKQVLDGIRTDLRGTSS
 1059

Query: 353 TNEVGDAI 360
 T EVGDAI
 Sbjct: 1060TTEVGDAI 1083

Candida seq orf10262:179916-178795**1**

VKTKTITVLPGDHVGTEIVNEAIKVLKAIEAATPYQKIQFDFKHHLIGGAIDATGVPLPDDALESASKS
 SDAVLLGAVGGPKWGTGTVRPEQGLLKIRKELNLYANIRPCNFASDSLLELSPLKAEVVKGTNLIIVRE
 LVGGIYFGERQEQESEDKKTAWDTEKYTVDEVTRITRMAAFMALQHNPPPLPIWSLDKANVLASSRLWR
 KTVDKVISEEFPAHSVQHQLIDSAAMILIQNPTKLNGLIITSNMFGDIISDEASVIPGSLGLLPSASLA
 SLPDTNTAFGLYEPCHGSAPDLPANKVNPIATILSAASMLRLSLDCVKEAEAEAEAVKQVLDGIRTDLRGTSS
 LRGTTSS1060TTEVGDAI

FIGURE 18

BLAST OF SEQ ID NO:36 AGAINST:

Elrond pep

A. nidulans

>AnrP4374925 LE3B_ASPNG 3-isopropylmalate dehydrogenase B (Beta-IPM

dehyd

Length = 370

Score = 597 bits (1540), Expect = e-171

Identities = 295/364 (81%), Positives = 326/364 (89%), Gaps = 1/364 (0%)

Query: 4 TYNILVLPDGGIGPEVMT EAVKVLKVFENEHRKFNL RQELIGGCSIDAHGKSVTEEVKKA 63
 +YNILVLPDGGIGPEVM EA K+L +F +F + ELIGGCSID HGKSVT+ V A
 Sbjct: 5 SYNILVLPDGGIGPEVMAEATKILSLFNTSTVRFRTQT ELIGGCSIDTHGKSVTQAVLDA 64

Query: 64 ALESDAVLFAAVGGPKWDHIRRGLDGP EGGLLQVRKAMDIYANLRPCSASSPSASIAKEF 123
 A+ SDAVLFAAVGGPKWDHIRRGLDGP EGGLLQ+RKAMDIYANLRPCS SPS IA++F
 Sbjct: 65 AVSSDAVLFAAVGGPKWDHIRRGLDGP EGGLLQVRKAMDIYANLRPCSV DSPSREIARDF 124

Query: 124 SPFRQEVIEGVDFV VVRENC GGAYFGKKIEEDYAMDEWGY SEREIQRITRLSAEIALRH 183
 SPFRQ+VIEGVDFV VVRENC GGAYFGKK+EE+DYAMDEWGY S EIQRITRLSAE+ALRH
 Sbjct: 125 SPFRQDVIEGVDFV VVRENC GGAYFGKKVEEDYAMDEWGY SASEIQRITRLSAELALRH 184

Query: 184 NPPWPVISL DKANVLASSRLWRRVVEKTM TTEYPQVKLVHQLADSASLILATNP RALNGV 243
 +PPWPVISL DKANVLASSRLWRRVVEKTM+ EYPQVKLVHQLADSASLI+ATNP RALNGV
 Sbjct: 185 DPPWPVISL DKANVLASSRLWRRVVEKTMSE EYPQVKLVHQLADSASLIMATNP RALNGV 244

Query: 244 ILADNTFGDMISDQAGSIVGTLGVLPSASLDGLPSE-TRKRTNGLYEP THGSAPT IAGQN 302
 ILADNTFGDM+SDQAGS+VGTLGVLPSASLDGLP +++ +GLYEP THGSAPT IAG+N
 Sbjct: 245 ILADNTFGDMVSDQAGSLVGTLGVLPSASLDGLPKPGEQRKVHGLYEP THGSAPT IAGKN 304

Query: 303 IANPVAMILCVALMFRYS LDMETEAQRIE KAVQGVLDAGIRTPDLGGKSGTNEVGDAIVA 362
 IANP AMILCVALMFRYS +ME EA++IE AV+ VLD GIRT DLGG +GT E GDA+VA
 Sbjct: 305 IANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVLDKGIRTS DLGGSTGTREFGDAVVA 364

Query: 363 ALQG 366
 AL+G
 Sbjct: 365 ALKG 368

>AnrP4374925 niger seq

MSEKSYNILVLPDGGIGPEVMAEATKILSLFNTSTVRFRTQT ELIGGCSIDTHGKSVTQA
 VLDAAVSSDAVLFAAVGGPKWDHIRRGLDGP EGGLLQVRKAMDIYANLRPCSV DSPSREI
 ARDFSPFRQDVIEGVDFV VVRENC GGAYFGKKVEEDYAMDEWGY SASEIQRITRLSAEL
 ALRHDPPWPVISL DKANVLASSRLWRRVVEKTMSE EYPQVKLVHQLADSASLIMATNPRA
 LNGVILADNTFGDMVSDQAGSLVGTLGVLPSASLDGLPKPGEQRKVHGLYEP THGSAPT I
 AGKNIANPTAMILCVALMFRYSFNMEAEARQIEAAVRTVLDKGIRTS DLGGSTGTREFGD
 AVVAALKGEL

FIGURE 19

BLAST OF SEQ ID NO:36 AGAINST:

BLASTP:temp job2 pep 6 AnrP3711474
 >AnrP3711474 hypothetical protein [Aspergillus oryzae]
 Length = 364

Score = 375 bits (963), Expect = e-104
 Identities = 195/367 (53%), Positives = 260/367 (70%), Gaps = 10/367 (2%)

Query: 2 VTTYNILVLPDGGIGPEVMTEAVKVLKVFE-NEHRKFNLQELIGGCSIDAHGKSVTEEV 60
 +++YNI+V GD GPEV EA+KVL+ E N FNL+ L+GG SIDA G +T+E
 Sbjct: 1 MSSYNIVVFGGDHCGPEVTAEAIKVLRAVEKNRDVTFNLQDHLGGASIDATGSPLTDEA 60

Query: 61 KKAALSDAVLFAAVGGPKWDHIRGLDPEGGLQLRKAMDIYANLRPCSASSPSASIA 120
 AA +DAVL A+GGPKW G PE G+L+LRK M + NLRPC+ ++PS
 Sbjct: 61 LNAAKNADAVLLGAIGGPKWG---TGAVRPEQGILKLRKEMGTFGNLRPCNFAAPSLV-- 115

Query: 121 KEFSPFRQEVIEGVDFVVRVRENCGGAYFGKKIEEED--YAMDEWGYSEREIQRITRLSAE 178
 E SP R +V GV+F ++RE GG YFG++ E++ YAMD YS EI+RI RL+A
 Sbjct: 116 -ESSPLRADVCRGVNFNIIRELTGGIYFGERKEDDGSYGAMDTPEYSRAEIERIIRLAH 174

Query: 179 IALRHNPPWPVISLIDKANVLASSRLWRRVVEKMTTTEYPQVKLVHQLADSASLILATNPR 238
 +AL+H+PP PV SLDKANVLA+SRLWR+VV + M E+PQ+K+ HQL DSA++I+ NPR
 Sbjct: 175 LALQHDPPPLPVWSLIDKANVLATSRLWRKVVTEVMAKEFPQLKIEHQLIDSAAMIMVKNPR 234

Query: 239 ALNGVILADNTFGDMISDQAGSIVGTGLVLPASLDGLPSETRKRTNGLYEPHGSAPT I 298
 LNG+++ N FGD+ISD+A I G+LG+LPSASL G+P + + NG+YEP HGSAP I
 Sbjct: 235 QLNGIVVTSNLFGLDIISDEASVIPGSLGLLPSASLSGIP-DGNSKVNGIYEPHGSAPDI 293

Query: 299 AGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDA GIRT PDLGGKSGTNEVGD 358
 AG+ I NPVA IL VA+M +YS + EA+ IE+AV V+++G+RT D+GGK+ T EVGD
 Sbjct: 294 AGKGIVNPVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDIGGKATTAEVGD 353

Query: 359 AIVAALQ 365
 A+ A L+
 Sbjct: 354 AVAAELE 360

Oryzae seq >AnrP3711474
 MSSYNIVVFGGDHCGPEVTAEAIKVLRAVEKNRDVTFNLQDHLGGASIDATGSPLTDEA
 LNAAKNADAVLLGAIGGPKWGTGAVRPEQGILKLRKEMGTFGNLRPCNFAAPSLVESSPL
 RADVCRGVNFNIIRELTGGIYFGERKEDDGSYGAMDTPEYSRAEIERIIRLAH LALQHD
 PPLPVWSLIDKANVLATSRLWRKVVTEVMAKEFPQLKIEHQLIDSAAMIMVKNPRQLNGIV
 VTSNLFGLDIISDEASVIPGSLGLLPSASLSGIPDGNSKVNGIYEPHGSAPDIAGKGIVN
 PVAAILSVAMMMQYSFGLFAEARAIEQAVSNVIESGVRTGDIGGKATTAEVGD AVAAELE
 KLLK

FIGURE 20

BLAST OF SEQ ID NO:36 AGAINST:

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┌ BLASTP:temp_job2_pep_9_AnP4379986
>AnP4379986 conserved hypothetical protein [Aspergillus nidulans
  FGSC A4
  Length = 357

Score = 149 bits (376), Expect = 1e-36
Identities = 113/369 (30%), Positives = 186/369 (49%), Gaps = 27/369 (7%)

Query: 1  MVTYNYLVLPDGDGIGPEVMTAEVVKLVKFENEHRKFNLRQELIGGCS--IDAHGKSVTE 58
          M  TY I  +P DGIGPEV+   V VLK  ++ + F+L    +   S   A GK + +
Sbjct: 1  MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQSFSLDFTHLDWSSETFKATGKYIPD 60

Query: 59  EVKKAALSDAVLFAAVGGPKW-DHIRRLDGPPEGGLQLRKAMDIYANLRPCSASSPSA 117
          +   ++DA+LF AVG P   DHI          G  L + +   YAN+R       P+
Sbjct: 61  GGLEVLKKNDAILFGAVGAPDVPDHISLW-----GLRLAICQPFQYANVR-----PTR 109

Query: 118  SIAKEFSPPRQEVIEGVDFVVVRENCGGAYFGK-----KIEEEDYAMDEWGYSEREIQRI 172
          +   SP R+   +D+V+VREN  G Y G+   +   + A +   +S + ++RI
Sbjct: 110  VLRGTQSPLRKCNTGDLDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVVERI 169

Query: 173  TRLSAEIALRHNPWPVVISLDKANVLASSRLWRRVVEKTMTEYPQVKLVHQLADSASLI 232
          R + E A + P   + + K+N   + +   V   + ++P+V +   L D+ +
Sbjct: 170  MRFAFETAAK-RPRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTR 228

Query: 233  LATNPRALNGVILADNTFGDMISDQAGSIVGTLGVLPASLDGLPSETRKRTNGLYEPH 292
          +   P +L+  I+A N   D++SD A ++ G++G+ P+++LD   ++   ++EP H
Sbjct: 229  MVLKPESLD-TIVASNLHADILSDLAALAGSIGIAPTSNLD-----PTRQNPSMFEPH 282

Query: 293  GSAPTIAGQNIANPVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAGIRTPDLGGKSG 352
          GSA  I G+ IANPVA   A M + L + A ++ + V+ V ++GI T DLGG +
Sbjct: 283  GSAFDITGKGIANPVATFWTAAEMLEW-LGEKDAADKLMQCVESVCESGILTADLGGTAT 341

Query: 353  TNEVGDAIV 361
          T EV  A+V
Sbjct: 342  TKEVTSADV 350

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Nidulans seq >AnP4379986
MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQSFSLDFTHLDWSSETFKATGKYIPD
GGLEVLKKNDAILFGAVGAPDVPDHISLWGLRLAICQPFQYANVRPTRVLRGTQSPLRK
CNTGDLDWVIVRENSEGEYAGQGGRSHRGHPWEVATEVAIFSRQGVVERIMRFAFETAAKR
PRKLLTVVTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTRMVLKPESLDTIV
ASNLHADILSDLAALAGSIGIAPTSNLDPTRQNPSMFEPHGSAGFDITGKGIANPVATF
WTAAEMLEWLGEKDAADKLMQCVESVCESGILTADLGGTATTKEVTSADVVEINRLN

```

FIGURE 21

BLAST OF SEQ ID NO:36 AGAINST:

>gnl|TIGR_222929|contig:1772:c_posadasii Coccidioides posadasii C735
 unfinished fragment of genome
 Length = 119053

Score = 286 bits (732), Expect(2) = e-128
 Identities = 146/233 (62%), Positives = 173/233 (74%), Gaps = 24/233 (10%)
 Frame = -3

Query: 160 AMDEWGYSTTEIQXXXXXXXXXXXXHDPWPVISLTKANVLASSRLWRRVVENTISVEYP 219
 AMDEWGYST E+Q HDPPWPVIS+DKANVLASSRLWRRVVE T++ E+P
 Sbjct: 33806 AMDEWGYSTQEVQRIARLAHVALRHDPWPVISMDKANVLASSRLWRRVVEKTLTTEFP
 33627

Query: 220 QVKLVHQLADSASLIMATDPRLNGVILADNTFGDMLSDQAGSLIGTLGVLPSASLDGLP 279
 QVK HQLADSASLIMAT+PR LNGV+LADNTFGDMLSDQAGS++G+LGVLPASL G+P
 Sbjct: 33626 QVKFSQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLGVLPASLSGIP
 33447

Query: 280 HPGKQE--KVRGLYEPTHGSAPT-----IAGKNIANPTAMILC 315
 +++ K LYEPTHGSAPT IAGKN+ANP AMILC
 Sbjct: 33446 GEKRKDGKKSALYEPTHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILC
 33267

Query: 316 VSLMFRYSFNMENEARQIEDAVRAVLDRGLRTPDLGGNSSTQEFDAVVAALQ 368
 V++MFRYSFNM E+ IE+AV A L+ G+RTPDLGG + T + G+A+VA ++
 Sbjct: 33266 VAMMFRYSFNMPEAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHK 33108

Query: 4 TRAYNILVLPDGDIGPEVMAEAIKVLRTFNSSMQFHLQEELIGGISIDTHGHSVTQPPX 63
 ++ YNIL LPGDGDIGPE+MAEAIKVL+ F+S ++ F+L+ ELIGG S'D HG +T
 Sbjct: 34383 SKTYNILTLPDGDIGPEIMAEAIKVLQAFSSPNLNFNLNELIGGCSIDAHGTPITDAVK
 34204

Query: 64 XXXXXXXXXXXXXXXGSKVDHIRGLDGPEGGLLQVRKAMDIYANLRPCSVDVPSREIAR 123
 GG K D RRGL+GPEGGLLQ+RK +D+Y N+RPCS DV ++R
 Sbjct: 34203 QAALESDAVLFAVGGPKWDSSRRGLEGPEGGLLQLRKVLVDVYGNVRPCSTDV-CASVSR
 34027

Query: 124 DFSPFRQEVIEGVDFVVRRENCGAYFGKKVEEENY 159
 +FSP+R EV+EGVDFVV+RENCGAYFGK VE+E+Y
 Sbjct: 34026 EFSPYRTEVVEGVDFVVRRENCGAYFGKXVEDEDY 33919

Coccidioides

2

SKTYNILTLPDGDIGPEIMAEAIKVLQAFSSPNLNFNLNELIGGCSIDAHGTPITDAVKQAALESDAVLFAVGGPKWDSSRRGLEGPEGGLLQLRKVLVDVYGNVRPCSTDVCASVSREFSPYRTEVVEGVDFVVLRENCGAYFGKXVEDEDYAMDEWGYSTQEVQRIARLAHVALRHDPWPVISMDKANVLASSRLWRVVEKTLTTEFPQVKFSQLADSASLIMATNPRSLNGVLLADNTFGDMLSDQAGSIVGSLGVLPASLSGIPGEKRKDGKKSALYEPTHGSAPT*VNCDLWMINTARKANRLD*CRIAGKNVANPLAMILCVAMMFRYSFNMPEAKAIENAVTATLEAGIRTPDLGGKAGTTDVGNAIVAHK

FIGURE 22

SEQ ID NO:36 against: Cryptococcus >chr01b.b3501.031220.C11
(289426 bp) Length = 289426

Score = 183 bits (465), Expect(3) = 3e-68 Frame = +3
Identities = 113/258 (43%), Positives = 144/258 (55%), Gaps = 39/258 (15%)

Query: 148 FGKKIE--EEDYAMDEWGYSEREIQRITRLSAEIALRHNPPFWFVISLDKANVLASSRLWR 205
FG++ E +E A D+ YS+ EI+RITR++A+IAL PP P+ S+DRANVLA+SRLWR
Sbjct: 173334 FGERQETNDEGVAWDQCIYSKPEIERITRVAAQIALAAEPPLPITSVDKANVLATSRLWR 173513

Query: 206 RVVEKTMTEYPQVKLVHQLADSASLILATNPRALNGVILADNTFGDM----- 253
+ V + M EYPQ+KL HQL DSA++I+ NPR LNGV+L +N FGDM
Sbjct: 173514 KTVSELMAKEYPQLKLEHQLVDSAAIMIMIANPRKLNGLVLTENMFGDM*VLSMVTKYRC* 173693

Query: 254 -----ISDQAGSIVGTGLGVLPASLDGLPSETRKRTNGLYE-----PTHGS 294
S A + L + P LP ++ HGS
Sbjct: 173694 VCVVFLTRAPSSPAPLVSSLLRLSPVPPILSLPFWVMSRSTSIFFFLTYFN*PLCSIHGS 173873

Query: 295 APTIAGQNIANFVAMILCVALMFRYSLDMETEAQRIEKAVQGVLDAG-----IRTPDLG 348
AP IAGQ IANP+ IL A+M RYSL EA IE+AVQ VLD+ RT DLG
Sbjct: 173874 APDIAGQGIANPIGTILSAAMMLRYSLGKREAAIEQAVQKVLDASAESGGFDYRTKDLG 174053

Query: 349 GKSGTNEVGDAIVAALQG 366
G+ T EVGD +V L+G
Sbjct: 174054 GQRSTKEVGDKVVEVLKG 174107

Query: 15 IGPEVMTEAVKVLKVFENEHR-KFNLRQELIGGCSIDAHGKSVTEEVKKALESDAVLFA 73
IGPEV+ EAV+VL+ N K +L+ GG +ID HG + +E KA E+DAVL
Sbjct: 172844 IGPEVVAEAVRVLETIVNHSDDLKLDLKSDFGGAAIDNHGVPLPDETLLKACREADAVLMG 173023

Query: 74 A-----VGGPKWDHIRRGLDGPEGGLLQLRKAMDIYANLRPCSASSPS 116
A VGGPKW G PE G+L+LRK + +YAN+RP A+ S
Sbjct: 173024 ACDFLAIRIKS*TA*KGSVGGPKWGV---GPVRPEQGILKRLKELGLYANIRP--ANFAS 173188

Query: 117 ASIAKEFSPPRQEVIEGVDFVVRNCGG 145
S+ K SP +++ G D +V+RE GG
Sbjct: 173189 ESLLKR-SPLKEDTARGTDIIVLRELIGG 173272

Query: 244 ILADNTFGDMISDQAGSIVGTGLGVLPASLD-----GLPS---ETRRKRTNGLYEPTH 292
+L + +GD++SD + ++G LG+ PS ++ G PS K ++E H
Sbjct: 238292 LLIPHRYGDLSDLSAGLIGGLTSPSGNIGKVSLSHDYGSPSIELTGDK*DA SIFEAVH 238471

Query: 293 GSAPTIAGQNIANFVAMILCVALMFR----- 318
GSAP I G+ +ANP A++L +M R
Sbjct: 238472 GSAPDIEGKGLANPTALLSSLMMLR*VTQIPSVIVPALYSPVDPHTHPLARNVADLFVH 238651

Query: 319 YSLDMETEAQRIEKA---VQG-----VLDAGIRTPDLGGKSGTNEVG 358
+ + A +IEKA V G + + T DLGGK+GT E D
Sbjct: 238652 RHMSLYELADKIEKAALSVSGTFWLFHTFEMLIQVS*TIAEGKAITRDLGGKAGTKEYTD 238831

Query: 359 AIVAAL 364
AI++ L
Sbjct: 238832 AILSKL 238849

Query: 95 LQLRKAMDIYANLRPCSASSPSASIAKEFSPPRQEVIEGVDFVVRNCGGAYFGKKIEE 154
L LR+ ++AN+RPC SI +P+ + V+ V++REN G Y G IE
Sbjct: 237609 LTLRRTFSLEFANVRPC-----VSIKGYKTPY-----DNVNTVLIRENTEGEYSG--IEH 237749

Query: 155 E 155
E
Sbjct: 237750 E 237752

Query: 5 YNIVLPGDGIGPEVMTEAVKVLK 28
Y + ++PGDGIGPE+ ++ K
Sbjct: 237256 YTVTLIPGDGIGPEIANSVKQIFK 237327

Query: 4 TYNIVLPGDGIG 16
++ I VLPDGIG
Sbjct: 172752 SFKITVLPDGIG 172790

FIGURE 23

Clustalw of sequences of figure 18-22

```
! Sequence: BLASTP:temp_job2_pep_4_AnRP4374925  nidulans (see figure 19)
! Sequence: BLASTP:temp_job2_pep_6_AnRP3711474  oryzae (see figure 20)
! Sequence: BLASTP:temp_job2_pep_9_AnRP4379986  nidulans (see figure 21)
! Sequence: USERPROTEIN:1_job6_1  candida (see figure 18)
! Sequence: USERPROTEIN:2_job7_2  coccidioides (see figure 22)
CLUSTAL W (1.82) multiple sequence alignment
```

```
temp_job2_pep_4_AnRP4374925  ---SYNILVLPGDGIGPEVMAEATKILSLFNTST---VRFRTQTELIGG
temp_job2_pep_6_AnRP3711474  -MSSYNIVVFGGDHCGPEVTAEAIKVLRAVEKNR---DVTFNLDHLLGG
temp_job2_pep_9_AnRP4379986  MAKTYRIATIPADGIGPEVIDAGVIVLKALADKLQS--FSLDFTHLDWSS
1_job6_1                    -VKTKTITVLPGDHVGTEIVNEAIKVLKAIEAATPYQKIQFDFKHHLIGG
2_job7_2                    -SKTYNILTLPGDGIGPEIMAEAIKVLQAFSSPN----LNFNLRNELIGG
                               :  *  .:  .*  *.:  .  :*  .  .  :  ..

temp_job2_pep_4_AnRP4374925  CSIDTHGKSVTQAVLDAVSSDAVLFAAVGGPKWDHIRRGLDGPPEGGLLQ
temp_job2_pep_6_AnRP3711474  ASIDATGSPLTDEALNAAKNADAVLLGAIGGPKWG---TGAVRPEQGILK
temp_job2_pep_9_AnRP4379986  ETFKATGKYIPDGGLEVLKKNDAILFGAVGAPDVP---DHISLWGLRLA
1_job6_1                    AAIDATGVPLPDDALESAKSSDAVLLGAVGGPKWG---TGTVRPEQGILLK
2_job7_2                    CSIDAHGTPITDAVKQAALSDAVLFASVGGPKWDSSRRGLEGPEGGLLQ
                               :::  *  :::  :  .  **:*:::*.*.  .  *

temp_job2_pep_4_AnRP4374925  VRKAMDIYANLRPCSVDSPSREIARDFSPFRQDVIEGVDFVVVRENCGGA
temp_job2_pep_6_AnRP3711474  LRKEMGTFGNLRPCNFAAPSL---VESSPLRADVCRGVNFNIIIRELTGGI
temp_job2_pep_9_AnRP4379986  ICQPFQQYANVRPTRVLRGTQ-----SPLRKCNTGDLDWVIVRENSEGE
1_job6_1                    IRKELNLYANIRPCNFASDSL---LELSPLKAEVVKGTNLIIVRELVGGI
2_job7_2                    LRKVLDVYGNVRPCSTDVCAS-VSREFSPYRTEVVEGVDFVVLRENCGGA
                               :  :  :  .:.*:**  :  **  :  .  :  ::**  *

temp_job2_pep_4_AnRP4374925  YFG-----KKVEEDDYAMDEWGYSAIEIQRITRLSAELALRHDPWPVIS
temp_job2_pep_6_AnRP3711474  YFGERKEDDGSG---YAMDTEPYSRAEIERIIRLA AHLALQHDPPLPVWS
temp_job2_pep_9_AnRP4379986  YAGQGGRSHRGHPWEVATEVAIFSRQGVERIMRFAFETAAGR-PRKLLTV
1_job6_1                    YFGERQEQEESDKKTAWDTEKYTVDEVTRITRMAAFMALQHNPLPIWS
2_job7_2                    YFG-----KXVEDEDYAMDEWGYSTQEVQRIARLAHVALRHDPWPVIS
                               *  *  .  *  :  ::  :  **  *::  *  ::  *
```

FIGURE 24


```
temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2
```

```
LDKANVLASSRLWRRVVEKTMSEEYPQVKLVHQLADSASLIMATNPRLN
LDKANVLATSRLWRKVVEVMAKEFPQLKIEHQLIDSAAMIMVKNPQRLN
VTKSNAQRNGMVLWDEVANIVAKDFPEVTMDKMLVDAMTTRMVLKPESLD
LDKANVLASSRLWRKTVDKVI SEEFPAHSVQHQLIDSAAMILIQNPTKLN
MDKANVLASSRLWRRVVEKTLTTEFPQVKFSHQLADSASLIMATNPRLN
: * * . . . : * : : : * : : : * : : : * *
```

```
temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2
```

GVLADNTFGDMVSDQAGSLVGTLGVLPSASLDGLP--KPGEQRKVHGLY
GIVVTSNLFGDIISDEASVIPGSLGLLPSASLSGIP----DGNSKVNIGIY
-TIVASN LHADI LSDLAAALAGSIGIAPTSNLDPTR-----QNPSMF
GIIITSNMFGDIISDEASVIPGSLGLLPSASLASLP---DTN-TAFGLY
GVLLADNTFGDMLSDQAGSIVGSLSGLVPSASLSGIPGEKRKD GKSYLY

: : . * . * : : * : : * : : * : : *

```
temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2
```

EPHGSAPT IAGKNIANPTAMILCVALMFYRSFNMEAEARQIEAAVRTVL
EPIHGSAPDIAGKGIVNPVAAILSVAMMMQYSFGLFAEARAIEQAVSNVI
EPIHGSAPFDITGKGIANPVATFWTAAEMLEWLG-EKDAADKLMQCVCESVC
EPCHGSAPDLPAN-KVNPIATI LSAASMLRLSLDCVKEAEALEEAVKQVL
EPHGSAPT-----
* * * * *

```
temp_job2_pep_4_AnRP4374925
temp_job2_pep_6_AnRP3711474
temp_job2_pep_9_AnRP4379986
1_job6_1
2_job7_2
```

DKGIRTSDLGGSTGTREFGDAVVAALKG
ESGVRTGDIGGKATTAEVGDAVAEELE-
ESGILTADLGGTATTKEVTSADV-----
DSGIRTADLRGTSSTTEVGDAI-----

FIGURE 25

Identification of peptides in AFC fractions.

Protein extract	CssI (AmrP440134)	Hydrophobin (AmrP57221)	GAPDH (AmrP539502)	Enolase (AmrP7789)	Catalases and IMDH B
Diffusate	KVAQELINPGPK	FPVPDDITVK ATYAADVTDIDEGILAGTLK	AGISLNPFFVK TAAQNTIPSSGAAK NILGYTEDDVVSSDLNGDER	NVNETIGPALIK VNQIGTLTESIQAAK TSDPQIVGDDLFTVTPGR	Not detected
Cell surface exposed	VAGELINPGPK	FPVPDDITVK ATYAADVTDIDEGILAGTLK	Not detected	Not detected	FGFDLIDPTK (Catalase B peptide AmrP977704) IX, AEX, ALR (IMDH B peptide)
Cell wall	KVAQELINPGPK VAGELINPGPK SISFQIDCR EGABQSAAPQAEHSTK VVTTPYPCDQVK	FPVPDDITVK 3-12 ATYAADVTDIDEGILAGTLK 30-50	AGISLNPFFVK TAAQNTIPSSGAAK NILGYTEDDVVSSDLNGDER VPTSNVSVVDLTCR YDTTHGQFK GTIEFYDQGLIVNGK	Not detected	TGPSLLEDQIAR (Catalase A peptide AmrP145557)
Peptides used for Ab production	KVAQELINPGPKVVT KEGAEGSAAPQAEHSTK	PVPDDITVKQATEKCGD ATYAADVTDIDEGIL	TEDDVVSSDLNGDERS FKGTIETYYDGLIVNGK	KNVNETIGPALIKENID TSDPQIVGDDLFTVTPGR	DEEDQLRFGFDLIDPTKI RIDNDLARRVARAIGV

FIGURE 26

Biochemical characteristics of Cssl.

	Complete	N-terminus	C-terminus
MW	28179.92	13960.38	14236.54
Residues	260	130	130
Strongly Basic (+) Amino Acids (K, R)	25	10	15
Strongly Acidic (-) Amino Acids (D, E)	33	9	24
Hydrophobic Amino Acids (A, I, L, F, W, V)	89	55	34
Polar Amino Acids (N, C, Q, S, T, Y)	70	36	34
Isoelectric Point	5.081	7.626	4.760
Charge at pH 7.0	-7.634	0.892	-8.617

FIGURE 27

Sequence of Polypeptides chosen for the production of multiple antigenic peptides and antisera against selected target proteins.

<u>Peptide name</u>	<u>Peptide sequence</u>	<u>Parental protein</u>	<u>Reactivity vs AfC*</u>	<u>Reactivity vs AfM*</u>
GAP-B-1	FKGTIETVDQGLVNGKK (SEQ ID NO:12)	GAPDH B	++	+++
GAP-B-2	TEDDVSSDLNGDERS (SEQ ID NO:11)	GAPDH B	+++	++
HYD-1	PVPDDITVKQATEKCGD (SEQ ID NO:9)	hydrophobin	++	+++
HYD-2	ATYAGDVTIDIEGL (SEQ ID NO:10)	hydrophobin	++	+
CAT-B-1	DEEDQLRFGFDLLDPTKIVP (SEQ ID NO:15)	Catalase B	++	++
CAT-B-2	RIDNDLARRVARAIGV (SEQ ID NO:16)	Catalase B	++	++
ENO-1	KNVNETTGPALIKENID (SEQ ID NO:13)	Enolase	++	-
ENO-2	TSDFOIVGDDLTVTNPGK (SEQ ID NO:14)	Enolase	-	+
Peptide 2	KEGAEQSAPQAEHSTK (SEQ ID NO:8)	CssI	+++	+++
Peptide 1	KVAQEINPGPKVVT (SEQ ID NO:7)	CssI	++	++

*Reactivity of sera raised against the peptide against the surface of AfC or AfM

FIGURE 28

Analysis of the ability of anti-IMDH B IgG to bind the surface of clinical isolates.

Strain Number	Original substratum	Pathogenicity (underlying disease):	Anti IMDH-B intensity	
			<u>Conidia</u>	<u>Mycelium</u>
Isolate 46640	Human Lung	Aspergilloma	++	++
IHEM 1246	Outdoor air	-----	+	+
IHEM 2494	Human sputum	Allergic Bronchopulmonar Aspergillosis	++	++
IHEM 2739	Human sinus	Mycotic sinusitis	++++	++
IHEM 2895	Human bronchoaspiration (fungal ball)	Bronchitis	+++	+
IHEM 3007	Human lung	Pulmonary aspergillosis	-	+++
IHEM 4184	Human lung biopsy	Aspergillosis (heart transplant)	-	++
IHEM 4185	Human bone	Aspergillosis (heart transplant)	-	++
IHEM 4187	Human bronchial secretions	Aspergillosis (liver transplant)	+	+
IHEM 4699	Human bronchoaspiration	Aspergillosis (bone marrow transplant)	++	+
IHEM 4750	Human lung from autopsy	Aspergillosis (liver transplant)	+++	ND
IHEM 4756	Human sputum	Aspergillosis (marrow transplant)	-	+

FIGURE 29

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